

I

SID 1 -  
100% hit

RESULT 1  
D84401

LOCUS D84401 42398 bp DNA PRI 20-NOV-1999

DEFINITION Homo sapiens genomic DNA, 43 kb segment from chromosome6, complete sequence.

ACCESSION D84401

VERSION D84401.1 GI:2401263

KEYWORDS HTG.

SOURCE Homo sapiens cell\_line:CGMI DNA, clone:519.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Kikuti,Y.Y., Tamiya,G., Ando,A., Chen,L., Kimura,M., Ferreira,E.,  
Tsuji,K., Trowsdale,J. and Inoko,H.

TITLE Physical mapping 220 kb centromeric of the human MHC and DNA  
sequence analysis of the 43-kb segment including the RING1, HKE6,  
and HKE4 genes

JOURNAL Genomics 42 (3), 422-435 (1997)

MEDLINE 97349110

REFERENCE 2 (bases 1 to 42398)

AUTHORS Kikuti,Y., Inoko,H., Ando,A., Kimura,M., Watanabe,K. and Shiina,T.

TITLE Physical map of 200 kb at the centromeric side of the human MHC  
region and sequence of 43 kb

JOURNAL Unpublished (1996)

REFERENCE 3 (bases 1 to 42398)

AUTHORS Inoko,H.

TITLE Direct Submission

JOURNAL Submitted (12-APR-1996) to the DDBJ/EMBL/GenBank databases.  
Hidetoshi Inoko, Tokai University School of Medicine, Molecular  
Life Science; Bohseidai, Isehara, Kanagawa 259-11, Japan  
(E-mail:hinoko@is.icc.u-tokai.ac.jp, Tel:0463-93-1121,  
Fax:0463-94-8884)

FEATURES Location/Qualifiers

source 1. .42398  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/cell\_line="CGMI"  
/chromosome="6"  
/clone="519"

BASE COUNT 10359 a 10487 c 10025 g 11527 t

ORIGIN

Query Match 100.0%; Score 19; DB 9; Length 42398;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggattgattccaaaaccc 19  
|||||||

Db 12736 GGGATTGATTCCAAAACCC 12754

RESULT 2  
HS1033B10

LOCUS HS1033B10 175737 bp DNA PRI 11-MAY-2001

SID 2 13,194-  
13,175

419  
42052

DEFINITION Human DNA sequence from clone RP5-1033B10 on chromosome 6p21.2-21.31 Contains the D6S2723E gene for DNA segment on chromosome 6 (unique, pseudogene) 2723 expressed sequence (BING5), the gene C6ORF11 for chromosome 6 open reading frame 11 (BING4), the B3GALT4 gene for UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase polypeptide 4, the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a HTATSF1 (HIV TAT specific factor 1) pseudogene, a pseudogene similar to zinc finger genes, the RING1 gene for ring finger protein 1, the FABGL gene for FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like protein, the HKE4 gene for HLA class II region expressed gene KE4, the RXRB (retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, a pseudogene similar to HLA DPA1 antigen, part of a pseudogene similar to HLA class II histocompatibility antigen, DP beta chain precursors (HLA-DPB2), a putative novel gene, seve>.

ACCESSION AL031228

VERSION AL031228.1 GI:3646023

KEYWORDS HTG; acyl-carrier-protein; B3GALT4; beta3-Galactosyltransferase; BING4; BING5; C6ORF11; COL11A2; collagen; CpG island; D6S2723E; F28D1.1; FABGL; HKE4; HKE6; HLA-DPA3; HLA-DPB2; KE4; retinoid X receptor beta; ribosomal protein; ring finger; RING1; RING2; RING5; RPS18; RXRB; SACM2L; short-chain alcohol dehydrogenase; zinc finger.

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 175737)

AUTHORS Tubby,B.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Sep 24, 1998 this sequence version replaced gi:3550015. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>  
 RP5-1033B10 is from the library RPCI-5 constructed by the group of  
 Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pCYPAC2

This sequence is the entire insert of clone RP5-1033B10.

FEATURES	Location/Qualifiers
source	1. .175737 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /map="p21.2-21.31" /clone="RP5-1033B10" /clone_lib="RPCI-5"
repeat_region	1. .61 /note="Alu repeat: matches 2. .62 of consensus"
repeat_region	63. .368 /note="AluSx repeat: matches 1. .299 of consensus"
repeat_region	374. .403 /note="Cheshire repeat: matches 2264. .2292 of consensus"
repeat_region	404. .708 /note="AluSq repeat: matches 1. .305 of consensus"
repeat_region	719. .1027 /note="AluJb repeat: matches 1. .303 of consensus"
repeat_region	1028. .1220 /note="Cheshire repeat: matches 2055. .2256 of consensus"
repeat_region	1227. .1583 /note="Cheshire repeat: matches 1. .376 of consensus"
gene	complement(1534. .1961) /gene="D6S2723E"
CDS	complement(1534. .1961) /gene="D6S2723E" /note="dJ1033B10.1 (DNA segment on chromosome 6 (unique, pseudogene) 2723 expressed sequence (BING5)) overlaps cICF0811 match: ESTs: Em:AW379285 match: proteins: Tr:O15214" /codon_start=1 /pseudo /evidence=not_experimental
repeat_region	1593. .1671 /note="MIR repeat: matches 162. .241 of consensus"
repeat_region	1962. .2265 /note="AluSg repeat: matches 1. .296 of consensus"
repeat_region	2305. .2609 /note="AluSx repeat: matches 1. .307 of consensus"
repeat_region	2749. .2926 /note="AluJb repeat: matches 1. .165 of consensus"
repeat_region	3009. .3297 /note="AluSg repeat: matches 1. .290 of consensus"
repeat_region	4125. .4385 /note="AluSx repeat: matches 20. .294 of consensus"
repeat_region	5020. .5113 /note="MIR repeat: matches 110. .214 of consensus"
mRNA	join(5237. .5553,5705. .5799,6368. .6463,6617. .6730, 6853. .7119) /gene="C6ORF11"

```

/note="match: ESTs: Em:AI204504 Em:BF338950 Em:CNSLT1DO1
Em:AW192492 Em:BG334317 Em:BG476159 Em:CNSLT1FLA"
/evidence=not_experimental
/product="dJ1033B10.2.1 (chromosome 6 open reading frame
11 (BING4))"
mRNA join(5237. .5553,5705. .5799,6368. .6463,6617. .7119)
/gene="C6ORF11"
/note="match: cDNAs: Em:AW193506 Em:AI524223 Em:AA627958"
/evidence=not_experimental
/product="dJ1033B10.2.2 (chromosome 6 open reading frame
11 (BING4), isoform 1)"
gene 5237. .7119
/gene="C6ORF11"
CDS join(5244. .5553,5705. .5799,6368. .6463,6617. .>7119)
/gene="C6ORF11"
/note="overlaps cICF0811"
/codon_start=1
/evidence=not_experimental
/product="dJ1033B10.2.2 (chromosome 6 open reading frame
11 (BING4), isoform 1)"
/protein_id="CAC38439.1"
/db_xref="GI:14041695"
/translation="MATSGLDHQLKIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVA
GMGDVVNIWAGQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGITSMLV
PGAGEPNFDGLESNPYRSRQRQEWKALLEKVPaelICLDPRALAEVDVISLEQKGK
KEQIERLGYDPQAKAPFQPKPKQKGRSSTASLVKRKRKVMDEEHRVNEHWGPGLPQA
APSCCLCLCPCPATSHSVPVSSPSPVPRTSRGRAFSSSIIRRRRPSPRGPGHLPWTDL
CAEPDSRVAWEQSLPKITCREMSVPWNKEVGAVWPLPQLGVDSCLLGWVGIKEESDFL
"
CDS join(5244. .5553,5705. .5799,6368. .6463,6617. .6730,
6853. .6951)
/gene="C6ORF11"
/note="overlaps cICF0811
match: proteins: Tr:O15213"
/codon_start=1
/evidence=not_experimental
/product="dJ1033B10.2.1 (chromosome 6 open reading frame
11 (BING4))"
/protein_id="CAC38438.1"
/db_xref="GI:14041694"
/translation="MATSGLDHQLKIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVA
GMGDVVNIWAGQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGITSMLV
PGAGEPNFDGLESNPYRSRQRQEWKALLEKVPaelICLDPRALAEVDVISLEQKGK
KEQIERLGYDPQAKAPFQPKPKQKGRSSTASLVKRKRKVMDEEHRDKVRQSLQQQHHK
EAKAKPTGARPSALDRFVR"
repeat_region 5838. .6062
/note="9 copies 25 mer 88% conserved"
misc_feature complement(6837. .7118)
/note="match: STS: Em:G23698"
polyA_signal 7094. .7099
/gene="C6ORF11"
polyA_site complement(7409)
/gene="B3GALT4"
mRNA complement(7409. .8846)
/gene="B3GALT4"
/note="match: cDNAs: Em:Y15061 Em:AB003478
match: ESTs: Em:AA365900 Em:H20531 Em:R40008 Em:AA987754

```

Em:AA662961 Em:AA878755 Em:H20623 Em:R13948"  
 /evidence=not\_experimental  
 /product="dJ1033B10.3 (UDP-Gal:betaGlcNAc beta  
 1,3-galactosyltransferase, polypeptide 4)"  
 gene complement(7409. .8846)  
 /gene="B3GALT4"  
 polyA\_signal complement(7416. .7421)  
 /gene="B3GALT4"  
 misc\_feature 7419. .7588  
 /note="match: STS: Em:G43302"  
 CDS complement(7671. .8807)  
 /gene="B3GALT4"  
 /note="match: proteins: Tr:O54904 Tr:O43825 Tr:O54905  
 Tr:O54906 Tr:Q24157"  
 /codon\_start=1  
 /evidence=not\_experimental  
 /product="dJ1033B10.3 (UDP-Gal:betaGlcNAc beta  
 1,3-galactosyltransferase, polypeptide 4)"  
 /protein\_id="CAA20230.1"  
 /db\_xref="GI:3820979"  
 /db\_xref="SPTREMBL:O96024"  
 /translation="MQLRLFRRLLLAALLLVIVWTLFGPSGLGEELLSLSIASLLPAP  
 ASGPPLALPRLLIPNQEACSGPGAPPFLILLVCTAPENLNQRNAIRASWGGLREARG  
 LRVQTLFLLGEPNAQHPVWGSQGSDLASESAAQGDILQAAFQDSYRNLTLLKTLGSLNW  
 AEKHCPMARYVLKTDVVYVNPVELVSELVLRGGRWGQWERSTEPQREAEQEGGQVLH  
 SEEVPLLYLGRVHWRVNPSTPGGRHRVSEEQWPHTWGPFPYPYASGTGYVLSASAVQL  
 ILKVASRAPLLPLEDVFGVVSARRGGLAPTQCVKLAGATHYPLDRCCYGFLLTSHRL  
 DPWKMQEAWKLVGSGDGERTAPFCSWFQGVLGILRCRAIAWLQS"

Query Match 100.0%; Score 19; DB 9; Length 175737;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gggattgattccaaaaccc 19  
 ||||||||||||||||  
 Db 55302 GGGATTGATTCCAAAACCC 55320

RESULT 3  
 AC040962/c  
 LOCUS AC040962 200548 bp DNA HTG 21-MAY-2000  
 DEFINITION Homo sapiens chromosome 18 clone RP11-602P21 map 18, WORKING DRAFT  
 SEQUENCE, 49 unordered pieces.  
 ACCESSION AC040962  
 VERSION AC040962.2 GI:7960461  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 200548)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 TITLE Homo sapiens chromosome 18, clone RP11-602P21  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 200548)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,  
 Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,  
 Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,  
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,  
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
 Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
 Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
 Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,  
 Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,  
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,  
 Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,  
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
 O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,  
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,  
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Direct Submission  
 Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 21, 2000 this sequence version replaced gi:7534164.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L9240  
 Center clone name: 602\_P\_21

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 177125 bases at least Q40  
 Consensus quality: 187777 bases at least Q30  
 Consensus quality: 192419 bases at least Q20  
 Insert size: 205000; agarose-fp  
 Insert size: 195748; sum-of-contigs  
 Quality coverage: 3.6 in Q20 bases; agarose-fp  
 Quality coverage: 3.7 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 49 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 1046: contig of 1046 bp in length  
 \* 1047 1146: gap of 100 bp  
 \* 1147 2330: contig of 1184 bp in length

*	2331	2430: gap of	100 bp
*	2431	3633: contig of	1203 bp in length
*	3634	3733: gap of	100 bp
*	3734	5263: contig of	1530 bp in length
*	5264	5363: gap of	100 bp
*	5364	6790: contig of	1427 bp in length
*	6791	6890: gap of	100 bp
*	6891	8653: contig of	1763 bp in length
*	8654	8753: gap of	100 bp
*	8754	10084: contig of	1331 bp in length
*	10085	10184: gap of	100 bp
*	10185	11548: contig of	1364 bp in length
*	11549	11648: gap of	100 bp
*	11649	13093: contig of	1445 bp in length
*	13094	13193: gap of	100 bp
*	13194	15199: contig of	2006 bp in length
*	15200	15299: gap of	100 bp
*	15300	16373: contig of	1074 bp in length
*	16374	16473: gap of	100 bp
*	16474	17628: contig of	1155 bp in length
*	17629	17728: gap of	100 bp
*	17729	20434: contig of	2706 bp in length
*	20435	20534: gap of	100 bp
*	20535	22597: contig of	2063 bp in length
*	22598	22697: gap of	100 bp
*	22698	24168: contig of	1471 bp in length
*	24169	24268: gap of	100 bp
*	24269	26029: contig of	1761 bp in length
*	26030	26129: gap of	100 bp
*	26130	28871: contig of	2742 bp in length
*	28872	28971: gap of	100 bp
*	28972	30650: contig of	1679 bp in length
*	30651	30750: gap of	100 bp
*	30751	34717: contig of	3967 bp in length
*	34718	34817: gap of	100 bp
*	34818	37374: contig of	2557 bp in length
*	37375	37474: gap of	100 bp
*	37475	40277: contig of	2803 bp in length
*	40278	40377: gap of	100 bp
*	40378	43104: contig of	2727 bp in length
*	43105	43204: gap of	100 bp
*	43205	46132: contig of	2928 bp in length
*	46133	46232: gap of	100 bp
*	46233	49208: contig of	2976 bp in length
*	49209	49308: gap of	100 bp
*	49309	52267: contig of	2959 bp in length
*	52268	52367: gap of	100 bp
*	52368	55880: contig of	3513 bp in length
*	55881	55980: gap of	100 bp
*	55981	59556: contig of	3576 bp in length
*	59557	59656: gap of	100 bp
*	59657	63372: contig of	3716 bp in length
*	63373	63472: gap of	100 bp
*	63473	65973: contig of	2501 bp in length
*	65974	66073: gap of	100 bp
*	66074	69877: contig of	3804 bp in length
*	69878	69977: gap of	100 bp

```

* 69978 74224: contig of 4247 bp in length
* 74225 74324: gap of 100 bp
* 74325 78685: contig of 4361 bp in length
* 78686 78785: gap of 100 bp
* 78786 83480: contig of 4695 bp in length
* 83481 83580: gap of 100 bp
* 83581 88260: contig of 4680 bp in length
* 88261 88360: gap of 100 bp
* 88361 91748: contig of 3388 bp in length
* 91749 91848: gap of 100 bp
* 91849 96938: contig of 5090 bp in length
* 96939 97038: gap of 100 bp
* 97039 101708: contig of 4670 bp in length
* 101709 101808: gap of 100 bp
* 101809 106565: contig of 4757 bp in length
* 106566 106665: gap of 100 bp
* 106666 114168: contig of 7503 bp in length
* 114169 114268: gap of 100 bp
* 114269 121428: contig of 7160 bp in length
* 121429 121528: gap of 100 bp
* 121529 129555: contig of 8027 bp in length
* 129556 129655: gap of 100 bp
* 129656 135298: contig of 5643 bp in length
* 135299 135398: gap of 100 bp
* 135399 143540: contig of 8142 bp in length
* 143541 143640: gap of 100 bp
* 143641 151858: contig of 8218 bp in length
* 151859 151958: gap of 100 bp
* 151959 161623: contig of 9665 bp in length
* 161624 161723: gap of 100 bp
* 161724 172118: contig of 10395 bp in length
* 172119 172218: gap of 100 bp
* 172219 180457: contig of 8239 bp in length
* 180458 180557: gap of 100 bp
* 180558 190268: contig of 9711 bp in length
* 190269 190368: gap of 100 bp
* 190369 200548: contig of 10180 bp in length.

```

# FEATURES

	Location/Qualifiers
source	1. .200548 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="18" /map="18" /clone="RP11-602P21" /clone_lib="RPCI-11 Human Male BAC"
misc_feature	1. .1046 /note="assembly_fragment"
misc_feature	1147. .2330 /note="assembly_fragment"
misc_feature	2431. .3633 /note="assembly_fragment"
misc_feature	3734. .5263 /note="assembly_fragment"
misc_feature	5364. .6790 /note="assembly_fragment"
misc_feature	6891. .8653 /note="assembly_fragment"



misc\_feature 8754. .10084  
 /note="assembly\_fragment"  
 misc\_feature 10185. .11548  
 /note="assembly\_fragment"  
 misc\_feature 11649. .13093  
 /note="assembly\_fragment"  
 misc\_feature 13194. .15199  
 /note="assembly\_fragment"  
 misc\_feature 15300. .16373  
 /note="assembly\_fragment"  
 misc\_feature 16474. .17628  
 /note="assembly\_fragment"

Query Match 100.0%; Score 19; DB 2; Length 200548;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gggattgattccaaaaccc 19  
 |||||  
 Db 63090 GGGATTGATTCCAAAACCC 63072

12481 ggtgaggat aaaaaactac acatttacag tgtacactcc tctgtgatg ggggcaccaa  
12541 aatctcagaa atcaccacta aataacttat tcatgtaact gaacaccacc tgtccccaa  
12601 aagcctattg aaaaaaaaaat tgaatacatg taggtctaga tataactctt gtgaagtatg  
12661 atattgattc tctatgtgt aatagatgga cattgaatac gagattatga atacaatcat  
12721 cctcagtatt caccaggat tgaattccaaa acccccactg atgttcaaac ccttgtata  
12781 acatggcata gtatttgcata ataacctatg cacatctcca catactttaa atcatcccta  
12841 ggttatctat ggtgcctatc gcaatgtaa tgctgtataa atatatgtta tactgtatt  
12901 ttatttga ttatttttc ttcttctet tcttcttc ccttccctc ctctctct  
12961 tcttcttc ctctcttct ttcttctga cagtctgct gtgtaccca ggctggagt  
13021 ctatggcagg atacagctc actgcaaact ctgctccca gggtcacgcc atttctctac  
13081 ctacgcctc caagtagctg ggattacagg tgcccgcac catgcccgcc taatttttt  
13141 gcatttttag tagagatggg gttcacgc gttagcagg atgtcttga tctctgact  
13201 ttgtatcca cccgcttga cctccaaag tgctgggatt acaggcgtga gccaccggc  
13261 ccgactggc catatatatt ttaaaaatat ttattctt cagtgggtg aatccatagg  
13321 tgtggaccta cagatacaaa atgccaactg tagttaatt ttataaaac tatctgtct  
13381 agtccattca gactgtata acaaaatacc ttactgag caattataa ataataaca  
13441 ctgcttacag ttctggagge tagaatgtcc aagcaggtgg tgccagcaga ttggtagcc  
13501 agtgaggga cacttgct catagatggc gcctcttgc tgcattca cgggtggaag  
13561 gggcaacaa gctccttgg gcctcttct ttaagacag ggtctcgtg tgcacctag  
13621 gctaagtga gtggcgtgat ctgggttac tgcaagctc gcctccagg ttcaagtga  
13681 tctctgct cagcctctg aatactggga ttacaaatgc ctgccaccat gactggctaa  
13741 ttttgtgt ttagtagag atggggttc tccatgtga ccaggctgt ctgaactac

D84401